

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: MURPHY, Dennis  
REID, John
- (ii) TITLE OF INVENTION: Alpha Glycosidase
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
CECCHI, STEWART & OLSTEIN
  - (B) STREET: 6 BECKER FARM ROAD
  - (C) CITY: ROSELAND
  - (D) STATE: NEW JERSEY
  - (E) COUNTRY: USA
  - (F) ZIP: 07068

- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.5 INCH DISKETTE
  - (B) COMPUTER: IBM PS/2
  - (C) OPERATING SYSTEM: MS-DOS
  - (D) SOFTWARE: ASCII

- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Unassigned
  - (B) FILING DATE: Concurrently
  - (C) CLASSIFICATION:

- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:

- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: HERRON, CHARLES J.
  - (B) REGISTRATION NUMBER: 28,019
  - (C) REFERENCE/DOCKET NUMBER: 331400-40

- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 201-894-1700
  - (B) TELEFAX: 201-994-1744

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
  - (A) LENGTH: 52 NUCLEOTIDES
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAATTTC ATTAAAGAGG AGAAATTAAC TATGAGAGCG CTCGTCCTTC AC

- (2) INFORMATION FOR SEQ ID NO:2:

0061903 071900

- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 31 NUCLEOTIDES  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGATCT AGGTTCCCCA TTTTCACCCC T

31

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 1,095 NUCLEOTIDES  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTG AGA GCG CTC GTC TTT CAC GGC AAC CTC CAG TAT GCC GAA ATC CCA  
 Leu Arg Ala Leu Val Phe His Gly Asn Leu Gln Tyr Ala Glu Ile Pro  
 5 10 15

48

AAG AGC GAA ATC CCA AAG GTC ATA GAG AAG GCA TAC ATC CCA GTC ATC  
 Lys Ser Glu Ile Pro Lys Val Ile Glu Lys Ala Tyr Ile Pro Val Ile  
 20 25 30

96

GAG ACA CTG ATT AAA GAA GAA ATT CCT TTT GGG CTC AAC ATA ACG GGC  
 Glu Thr Leu Ile Lys Glu Glu Ile Pro Phe Gly Leu Asn Ile Thr Gly  
 35 40 45

144

TAT ACC TTA AAG TTC CTC CCG AAG GAT ATT ATA GAC CTC GTT AAA GGG  
 Tyr Thr Leu Lys Phe Leu Pro Lys Asp Ile Ile Asp Leu Val Lys Gly  
 50 55 60

192

GGC ATC GCG AGT GAC CTG ATA GAG ATA ATC GGA ACG AGC TAC ACG CAC  
 Gly Ile Ala Ser Asp Leu Ile Glu Ile Ile Gly Thr Ser Tyr Thr His  
 65 70 75 80

240

GCA ATA CTC CCC CTC CTC CCG CTT AGC AGA GTA GAA GCA CAA GTT CAG  
 Ala Ile Leu Pro Leu Leu Pro Leu Ser Arg Val Glu Ala Gln Val Gln  
 85 90 95

288

AGA GAT AGG GAA GTT AAG GAA GAG CTC TTC GAG CTT TCT CCA AAG GGA  
 Arg Asp Arg Glu Val Lys Glu Glu Leu Phe Glu Val Ser Pro Lys Gly  
 100 105 110

336

TTC TGG CTG CCA GAG CTC GCC TAT GAC CCG ATA ATC CCT GCC ATA CTG 384  
Phe Trp Leu Pro Glu Leu Ala Tyr Asp Pro Ile Ile Pro Ala Ile Leu  
115 120 125

AAG GAC AAC GGT TAT GAG TAT CTA TTC GCC GAC GGG GAG GCG ATG CTT 432  
Lys Asp Asn Gly Tyr Glu Tyr Leu Phe Ala Asp Gly Glu Ala Met Leu  
130 135 140

TTC TCA GCT CAT CTC AAC TCG GCG ATA AAG CCA ATT AAA CCG CTC TAT 480  
Phe Ser Ala His Leu Asn Ser Ala Ile Lys Pro Ile Lys Pro Leu Tyr  
145 150 155 160

CCA CAC CTT ATA AAG GCC CAA AGG GAA AAG CGC TTT AGG TAC ATC AGC 528  
Pro His 3Leu Ile Lys Ala Gln Arg Glu Lys Arg Phe Arg Tyr Ile Ser  
165 170 175

TAT CTC CTT GGT CTC AGG GAG CTT AGG AAG GCG ATA AAG CTC GTT TTT 576  
Tyr Leu Leu Gly Leu Arg Glu Leu Arg Lys Ala Ile Lys Leu Val Phe  
180 185 190

GAA GGT AAG GTA ACG CTA AAG GCA GTC AAA GAC ATC GAA GCC GTA CCC 624  
Glu Gly Lys Val Thr Leu Lys Ala Val Lys Asp Ile Glu Ala Val Pro  
195 200 205

GTT TGG GTG GCC GTG AAC ACG GCT GTA ATG CTC GGC ATC GGA AGG CTT 672  
Val Trp Val Ala Val Asn Thr Ala Val Met Leu Gly Ile Gly Arg Leu  
210 215 220

CCT CTT ATG AAT CCT AAG AAA GTG GCG AGC TGG ATA GAG GAC AAG GAC 720  
Pro Leu Met Asn Pro Lys Lys Val Ala Ser Trp Ile Glu Asp Lys Asp  
225 230 235 240

AAC ATT CTT CTA TAC GGC ACC GAT ATA GAG TTC ATT GGC TAT AGG GAC 768  
Asn Ile Leu Leu Tyr Gly Thr Asp Ile Glu Phe Ile Gly Tyr Arg Asp  
245 250 255

ATT GCA GGC TAC AGA ATG AGT GTT GAG GGA TTA TTA GAG GTT ATA GAC 816  
Ile Ala Gly Tyr Arg Met Ser Val Glu Gly Leu Leu Glu Val Ile Asp  
260 265 270

GAG CTC AAC TCG GAA CTG TGC CTT CCC TCA GAG CTG AAG CAC AGT GGA 864  
Glu Leu Asn Ser Glu Leu Cys Leu Pro Ser Glu Leu Lys His Ser Gly  
275 280 285

AGG GAG CTC TAC TTA CGG ACT TCG AGT TGG GCA CCA GAT AAG AGC TTG 912  
Arg Glu Leu Tyr Leu Arg Thr Ser Ser Trp Ala Pro Asp Lys Ser Leu  
290 295 300

AGG ATA TGG AGA GAG GAA GGG AAC GCA AGA CTT AAT ATC CTG TCC 960  
 Arg Ile Trp Arg Glu Glu Gly Asn Ala Arg Leu Asn Met Leu Ser 320  
 305 315

TAC AAT ATG AGG GGC GAA CTC GCC CTT TTA GCC GAG AAC AGC GAT GCA 1008  
 Tyr Asn Met Arg Gly Glu Leu Ala Phe Leu Ala Glu Asn Ser Asp Ala 335  
 325 330

AGG GGA TGG GAG CCC CTC CCT GAG AGG AGG CTG GAT GCC TTC CGG GCG 1047  
 Arg Gly Trp Glu Pro Leu Pro Glu Arg Arg Leu Asp Ala Phe Arg Ala 350  
 340 345

ATA TAT AAC GAT TGG AGG GGT GAA AAT GGG GAA CCT TAG 1086  
 Ile Tyr Asn Asp Trp Arg Gly Glu Asn Gly Glu Pro End 365  
 355 360

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 364 AMINO ACIDS  
 (B) TYPE: POLYPEPTIDE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Arg Ala Leu Val Phe Met Gly Asn Leu Gln Tyr Ala Glu Ile 15  
 5 10  
 Phe Lys Ser Glu Ile Pro Lys Val Ile Glu Lys Ala Tyr Ile Pro 30  
 20 25  
 Val Ile Glu Thr Leu Ile Lys Glu Gln Ile Pro Phe Gly Leu Asn 45  
 35 40  
 Ile Thr Gly Tyr Thr Leu Lys Phe Leu Pro Lys Asn Ile Ile Asp 60  
 50 55  
 Leu Val Lys Gly Gly Ile Ala Ser Asp Leu Ile Glu Ile Ile Gly 75  
 65 70  
 Thr Ser Tyr Tyr His Ala Ile Leu Pro Leu Leu Pro Leu Ser Arg 90  
 80 85  
 Val Glu Ala Glu Val Gln Arg Asp Arg Glu Val Lys Glu Glu Leu 105  
 95 100  
 Phe Glu Val Ser Pro Lys Gly Phe Trp Leu Pro Glu Leu Ala Tyr 120  
 110 115  
 Asn Pro Ile Ile Phe Ala Ile Leu Lys Asp Asn Gly Tyr Glu Tyr 135  
 125 130  
 Leu Phe Ala Asp Gly Glu Ala Met Leu Phe Ser Ala His Leu Asn 150  
 140 145

Ser Ala Ile Lys Pro Ile Lys Pro Leu Tyr Pro His Leu Ile Lys 165  
 155  
 Ala Gln Arg Glu Lys Arg Phe Arg Tyr Ile Ser Tyr Leu Leu Gly 180  
 170  
 Leu Arg Glu Leu Arg Lys Ala Ile Lys Leu Val Phe Glu Gly Lys 195  
 185  
 Val Thr Leu Lys Ala Val Lys Asp Ile Glu Ala Val Pro Val Trp 210  
 200  
 Val Ala Val Asn Thr Ala Val Met Leu Gly Ile Gly Arg Leu Pro 225  
 215  
 Leu Met As? Pro Lys Lys Val Ala Ser Trp Ile Glu Asp Lys Asp 240  
 230  
 Asn Ile Leu Leu Tyr Gly Thr Asp Ile Glu Phe Ile Gly Tyr Arg 255  
 245  
 Asp Ile Ala Gly Tyr Arg Met Ser Val Glu Gly Leu Leu Glu Val 270  
 260  
 Ile Asp Glu Leu Asn Ser Glu Leu Cys Leu Pro Ser Glu Leu Lys 285  
 275  
 His Ser Gly Arg Glu Leu Tyr Leu Arg Thr Ser Ser Trp Ala Pro 300  
 290  
 Asp Lys Ser Leu Arg Ile Trp Arg Glu Asp Glu Gly Asn Ala Arg 315  
 305  
 Leu Asn Met Leu Ser Tyr Asn Met Arg Gly Glu Leu Ala Phe Leu 330  
 320  
 Ala Glu Asn Ser Asp Ala Arg Gly Trp Glu Pro Leu Pro Gln Arg 345  
 335  
 Arg Leu Asp Ala Phe Arg Ala Ile Tyr Asn Asp Trp Arg Gly Glu 360  
 350  
 Asn Gly Glu Pro

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